

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bazan, J. Fernando
- (ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 24-JUL-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/053,765
 - (B) FILING DATE: 25-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:
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 - (C) REFERENCE/DOCKET NUMBER: DX0758K1
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..567

Sequence Listing filed in USSN 09/122,443
For Reissue Application for Patent 6,060,284

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 64..567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CTG GGG AGC AGA GCT GTA ATG CTG CTG TTG CTG CTG CCC TGG ACA	48
Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr	
-21 -20 -15 -10	
GCT CAG GGC AGA GCT GTG CCT GGG GGC AGC AGC CCT GCC TGG ACT CAG	96
Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln	
-5 1 5 10	
TGC CAG CAG CTT TCA CAG AAG CTC TGC ACA CTG GCC TGG AGT GCA CAT	144
Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His	
15 20 25	
CCA CTA GTG GGA CAC ATG GAT CTA AGA GAA GAG GGA GAT GAA GAG ACT	192
Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr	
30 35 40	
ACA AAT GAT GTT CCC CAT ATC CAG TGT GGA GAT GGC TGT GAC CCC CAA	240
Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln	
45 50 55	
GGA CTC AGG GAC AAC AGT CAG TTC TGC TTG CAA AGG ATC CAC CAG GGT	288
Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly	
60 65 70 75	
CTG ATT TTT TAT GAG AAG CTG CTA GGA TCG GAT ATT TTC ACA GGG GAG	336
Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu	
80 85 90	
CCT TCT CTG CTC CCT GAT AGC CCT GTG GCG CAG CTT CAT GCC TCC CTA	384
Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu	
95 100 105	
CTG GGC CTC AGC CAA CTC CTG CAG CCT GAG GGT CAC CAC TGG GAG ACT	432
Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr	
110 115 120	
CAG CAG ATT CCA AGC CTC AGT CCC AGC CAG CCA TGG CAG CGT CTC CTT	480
Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu	
125 130 135	
CTC CGC TTC AAA ATC CTT CGC AGC CTC CAG GCC TTT GTG GCT GTA GCC	528
Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala	
140 145 150 155	
GCC CGG GTC TTT GCC CAT GGA GCA GCA ACC CTG AGT CCC TAA	570
Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro	
160 165	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr
-21 -20 -15 -10

Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
-5 1 5 10

Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
15 20 25

Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
30 35 40

Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
45 50 55

Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
60 65 70 75

Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
80 85 90

Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
95 100 105

Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
110 115 120

Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
125 130 135

Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
140 145 150 155

Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
160 165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 113..700

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 176..700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCTTAGAAG TCGGACTACA GAGTTAGACT CAGAACCAAA GGAGGTGGAT AGGGGGTCCA	60
CAGGCCTGGT GCAGATCACA GAGCCAGCCA GATCTGAGAA GCAGGGAACA AG ATG	115
Met	
-21	
CTG GAT TGC AGA GCA GTA ATA ATG CTA TGG CTG TTG CCC TGG GTC ACT	163
Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr	
-20 -15 -10 -5	
CAG GGC CTG GCT GTG CCT AGG AGT AGC AGT CCT GAC TGG GCT CAG TGC	211
Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln Cys	
1 5 10	
CAG CAG CTC TCT CGG AAT CTC TGC ATG CTA GCC TGG AAC GCA CAT GCA	259
Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His Ala	
15 20 25	
CCA GCG GGA CAT ATG AAT CTA CTA AGA GAA GAA GAG GAT GAA GAG ACT	307
Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu Thr	
30 35 40	
AAA AAT AAT GTG CCC CGT ATC CAG TGT GAA GAT GGT TGT GAC CCA CAA	355
Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro Gln	
45 50 55 60	
GGA CTC AAG GAC AAC AGC CAG TTC TGC TTG CAA AGG ATC CGC CAA GGT	403
Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln Gly	
65 70 75	
CTG GCT TTT TAT AAG CAC CTG CTT GAC TCT GAC ATC TTC AAA GGG GAG	451
Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly Glu	
80 85 90	
CCT GCT CTA CTC CCT GAT AGC CCC ATG GAG CAA CTT CAC ACC TCC CTA	499
Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser Leu	
95 100 105	
CTA GGA CTC AGC CAA CTC CTC CAG CCA GAG GAT CAC CCC CGG GAG ACC	547
Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu Thr	
110 115 120	
CAA CAG ATG CCC AGC CTG AGT TCT AGT CAG CAG TGG CAG CGC CCC CTT	595
Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro Leu	
125 130 135 140	
CTC CGT TCC AAG ATC CTT CGA AGC CTC CAG GCC TTT TTG GCC ATA GCT	643
Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile Ala	

145	150	155	
GCC CGG GTC TTT GCC CAC GGA GCA GCA ACT CTG ACT GAG CCC TTA GTG			691
Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val			
160	165	170	
CCA ACA GCT TAAGGATGCC CAGGTTCCCA TGGCTACCAT GATAAGACTA			740
Pro Thr Ala			
175			
ATCTATCAGC CCAGACATCT ACCAGTTAAT TAACCCATTA GGAAGTGTGC TGTTCCTGTT			800
TCGTTTGTGTT TGCCTGAAGG GCAAGGACAC CATTATTAAA GAGAAAAGAA ACAAACCCCA			860
GAGCAGGCAG CTGGCTAGAG AAAGGAGCTG GAGAAGAAGA ATAAAGTCTC GAGCCCTTGG			920
CCTTGGAAGC GGGCAAGCAG CTGCGTGGCC TGAGGGGAAG GGGGCGGTGG CATCGAGAAA			980
CTGTGAGAAA ACCCAGAGCA TCAGAAAAAG TGAGCCCAGG CTTTGCCCAT TATCTGTAAG			1040
AAAAACAAGA AAAGGGGAAC ATTATACTTT CCTGGGTGGC TCAGGGAAAT GTGCAGATGC			1100
ACAGTACTCC AGACAGCAGC TCTGTACCTG CCTGCTCTGT CCCTCAGTTC TAACAGAATC			1160
TAGTCACTAA GAACTAACAG GACTACCAAT ACGAACTGAC AAA			1203

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val		
-21 -20	-15	-10
Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln		
-5	1	5 10
Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His		
15	20	25
Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu		
30	35	40
Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro		
45	50	55
Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln		
60	65	70 75
Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly		
80	85	90

Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
 95 100 105
 Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
 110 115 120
 Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
 125 130 135
 Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
 140 145 150 155
 Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
 160 165 170
 Val Pro Thr Ala
 175

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu
 1 5 10 15
 Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
 20 25 30
 Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
 35 40 45
 Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
 50 55 60
 Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
 65 70 75 80
 Ser Leu Gln Ala Phe Val Ala Val Ala Ala Arg Val Phe Ala His Gly
 85 90 95
 Ala Ala Thr Leu Ser Gln
 100

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr	Pro	Leu	Gly	Pro	Ala	Arg	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	1	5	10	15
Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Ala	Asp	Gly	Ala	Glu	Leu	Gln	20	25	30	
Glu	Arg	Leu	Cys	Ala	Ala	His	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Met	35	40	45	
Leu	Leu	Arg	His	Ser	Leu	Gly	Ile	Pro	Gln	Ala	Pro	Leu	Ser	Ser	Cys	50	55	60	
Ser	Ser	Gln	Ser	Leu	Gln	Leu	Arg	Gly	Cys	Leu	Asn	Gln	Leu	His	Gly	65	70	75	80
Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Ala	Gly	Ile	Ser	85	90	95	
Pro	Glu	Leu	Ala	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Thr	Asp	100	105	110	
Phe	Ala	Thr	Asn	Ile	Trp	Leu	Gln	Met	Glu	Asp	Leu	Gly	Ala	Ala	Pro	115	120	125	
Ala	Val	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Thr	Phe	Thr	Ser	Ala	Phe	130	135	140	
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	Gln	Leu	His	Arg	Phe	145	150	155	160
Leu	Glu	Leu	Ala	Tyr	Arg	Gly	Leu	Arg	Tyr	Leu	Ala	Glu	Pro	165	170				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Pro Leu Gly Pro Thr Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15
Cys Leu Glu Gln Val Arg Lys Val Gln Ala Asp Gly Thr Ala Leu Gln
20 25 30
Glu Arg Leu Cys Ala Ala His Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45
Leu Leu Gly His Ala Leu Gly Ile Pro Gln Ala Pro Leu Ser Ser Cys
50 55 60
Ser Ser Gln Ala Leu Gln Leu Thr Gly Cys Leu Arg Gln Leu His Ser
65 70 75 80
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Ala Gly Ile Ser
85 90 95
Pro Glu Leu Ala Pro Thr Leu Asp Met Leu Gln Leu Asp Ile Thr Asp
100 105 110
Phe Ala Ile Asn Ile Trp Gln Gln Met Glu Asp Val Gly Met Ala Pro
115 120 125
Ala Val Pro Pro Thr Gln Gly Thr Met Pro Thr Phe Thr Ser Ala Phe
130 135 140
Gln Arg Arg Ala Gly Gly Thr Leu Val Ala Ser Asn Leu Gln Ser Phe
145 150 155 160
Leu Glu Val Ala Tyr Arg Ala Leu Arg His Phe Thr Lys Pro
165 170

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15
Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30
Glu Lys Leu Val Ser Glu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
35 40 45

Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
 50 55 60
 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln
 65 70 75 80
 Leu His Ser Gly Leu Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
 85 90 95
 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu
 100 105 110
 Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
 115 120 125
 Arg His Leu Ala Gln Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
 130 135 140
 Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
 145 150 155 160
 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
 165 170 175
 Pro

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Pro Leu Val Thr Val Ser Ala Leu Pro Pro Ser Leu Pro Leu Pro
 1 5 10 15
 Arg Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Ala
 20 25 30
 Ser Gly Ser Val Leu Leu Glu Gln Leu Cys Ala Thr Tyr Lys Leu Cys
 35 40 45
 His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Lys
 50 55 60
 Ala Ser Leu Ser Gly Cys Ser Ser Gln Ala Leu Gln Gln Thr Gln Cys
 65 70 75 80

Leu Ser Gln Leu His Ser Gly Leu Cys Leu Tyr Gln Gly Leu Leu Gln
 85 90 95
 Ala Leu Ser Gly Ile Ser Pro Ala Leu Ala Pro Thr Leu Asp Leu Leu
 100 105 110
 Gln Leu Asp Val Ala Asn Phe Ala Thr Thr Ile Trp Gln Gln Met Glu
 115 120 125
 Asn Leu Gly Val Ala Pro Thr Val Gln Pro Thr Gln Ser Ala Met Pro
 130 135 140
 Ala Phe Thr Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Ala Ile
 145 150 155 160
 Ser Tyr Leu Gln Gly Phe Leu Glu Thr Ala Arg Leu Ala Leu His His
 165 170 175
 Leu Ala

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ser Lys Asp Asp Ala
 1 5 10 15
 Thr Ser Asn Arg Pro Pro Leu Thr Ser Ala Asp Lys Met Glu Asp Phe
 20 25 30
 Ile Lys Phe Ile Leu Gly Lys Ile Ser Ala Leu Arg Asn Glu Met Cys
 35 40 45
 Asp Lys Tyr Asn Lys Cys Glu Asp Ser Lys Glu Val Leu Ala Glu Asn
 50 55 60
 Asn Leu Asn Leu Pro Lys Leu Ala Glu Lys Asp Arg Cys Phe Gln Ser
 65 70 75 80
 Arg Phe Asn Gln Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln
 85 90 95
 Glu Phe Gln Ile His Leu Lys Tyr Leu Glu Ser Asn Tyr Glu Gly Asn
 100 105 110
 Lys Asp Asn Ala His Ser Val Tyr Ile Ser Thr Lys His Leu Leu Gln

115	120	125
Thr Leu Arg Pro Met Asn Gln Ile Glu Val Thr Thr Pro Asp Pro Thr		
130	135	140
Thr Asp Ala Ser Leu Gln Ala Leu Phe Lys Ser Gln Asp Lys Trp Leu		
145	150	155
Lys His Thr Thr Ile His Leu Ile Leu Arg Arg Leu Glu Asp Phe Leu		
	165	170
		175
Gln Phe Ser Leu Arg Ala Ile Arg Ile Met		
180	185	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ala Thr Ser Asn Arg		
1	5	10
Leu Pro Leu Thr Pro Ala Asp Lys Met Glu Glu Leu Ile Lys Tyr Ile		
	20	25
		30
Leu Gly Lys Ile Ser Ala Leu Lys Lys Glu Met Cys Asp Asn Tyr Asn		
	35	40
		45
Lys Cys Glu Asp Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu		
50	55	60
Pro Lys Leu Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Gln		
65	70	75
		80
Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln Glu Phe Gln Ile		
	85	90
		95
Tyr Leu Lys Phe Leu Gln Asp Lys Tyr Glu Gly Asp Lys Glu Asn Ala		
	100	105
		110
Lys Ser Val Tyr Thr Ser Thr Asn Val Leu Leu Gln Met Leu Lys Arg		
115	120	125
Lys Gly Lys Asn Gln Asp Glu Val Thr Ile Pro Val Pro Thr Val Glu		
130	135	140
Val Gly Leu Gln Leu Ser Cys Ser His Arg Arg Val Ala Glu Ala His		
145	150	155
		160

Asn Asn His Leu Thr Leu Arg Arg Leu Glu Asp Phe Leu Gln Leu Arg
 165 170 175

Leu Arg Ala Val Arg Ile Met
 180

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Phe	Pro	Ala	Pro	Val	Pro	Pro	Gly	Glu	Asp	Ser	Lys	Asp	Val	Ala	1	5	10	15
Ala	Pro	His	Arg	Gln	Pro	Leu	Thr	Ser	Ser	Glu	Arg	Ile	Asp	Lys	Gln	20	25	30	
Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ile	Ser	Ala	Leu	Arg	Lys	Glu	Thr	Cys	35	40	45	
Asn	Lys	Ser	Asn	Met	Cys	Glu	Ser	Ser	Lys	Glu	Ala	Leu	Ala	Glu	Asn	50	55	60	
Asn	Leu	Asn	Leu	Pro	Lys	Met	Ala	Glu	Lys	Asp	Gly	Cys	Phe	Gln	Ser	65	70	75	80
Gly	Phe	Asn	Glu	Glu	Thr	Cys	Leu	Val	Lys	Ile	Ile	Thr	Gly	Leu	Leu	85	90	95	
Glu	Phe	Glu	Val	Tyr	Leu	Glu	Tyr	Leu	Gln	Asn	Arg	Phe	Glu	Ser	Ser	100	105	110	
Glu	Glu	Gln	Ala	Arg	Ala	Val	Gln	Met	Ser	Thr	Lys	Val	Leu	Ile	Gln	115	120	125	
Phe	Leu	Gln	Lys	Lys	Ala	Lys	Asn	Leu	Asp	Ala	Ile	Thr	Thr	Pro	Asp	130	135	140	
Pro	Thr	Thr	Asn	Ala	Ser	Leu	Leu	Thr	Lys	Leu	Gln	Ala	Gln	Asn	Gln	145	150	155	160
Trp	Leu	Gln	Asp	Met	Thr	Thr	His	Leu	Ile	Leu	Arg	Ser	Phe	Lys	Glu	165	170	175	
Phe	Leu	Gln	Ser	Ser	Leu	Arg	Ala	Leu	Arg	Gln	Met					180	185		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Glu Asp Phe Lys Asn Asp Thr
1 5 10 15
Thr Pro Ser Arg Leu Leu Leu Thr Thr Pro Glu Lys Thr Glu Ala Leu
20 25 30
Ile Lys His Ile Val Asp Lys Ile Ser Ala Ile Arg Lys Glu Ile Cys
35 40 45
Glu Lys Asn Asp Glu Cys Glu Asn Ser Lys Glu Thr Leu Ala Glu Asn
50 55 60
Lys Leu Lys Leu Pro Lys Met Glu Glu Lys Asp Gly Cys Phe Gln Ser
65 70 75 80
Gly Phe Asn Gln Ala Ile Cys Leu Ile Lys Thr Thr Ala Gly Leu Leu
85 90 95
Glu Tyr Gln Ile Tyr Leu Asp Phe Leu Gln Asn Glu Phe Glu Gly Asn
100 105 110
Gln Glu Thr Val Met Glu Leu Gln Ser Ser Ile Arg Thr Leu Ile Gln
115 120 125
Ile Leu Lys Glu Lys Ile Ala Gly Leu Ile Thr Thr Pro Ala Thr His
130 135 140
Thr Asp Met Leu Glu Lys Met Gln Ser Ser Asn Glu Trp Val Lys Asn
145 150 155 160
Ala Lys Val Ile Ile Ile Leu Arg Ser Leu Glu Asn Phe Leu Gln Phe
165 170 175
Ser Leu Arg Ala Ile Arg Met Lys
180

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Phe	Pro	Thr	Ser	Gln	Val	Arg	Arg	Gly	Asp	Phe	Thr	Glu	Asp	Thr	
1				5					10					15		
Thr	Pro	Asn	Arg	Pro	Val	Tyr	Thr	Thr	Ser	Gln	Val	Gly	Gly	Leu	Ile	
		20					25						30			
Thr	His	Val	Leu	Trp	Glu	Ile	Val	Glu	Met	Arg	Lys	Glu	Leu	Cys	Asn	
		35					40					45				
Gly	Asn	Ser	Asp	Cys	Met	Asn	Asn	Asp	Asp	Ala	Leu	Ala	Glu	Asn	Asn	
	50					55				60						
Leu	Lys	Leu	Pro	Glu	Ile	Gln	Arg	Asn	Asp	Gly	Cys	Tyr	Gln	Thr	Gly	
65				70						75					80	
Tyr	Asn	Gln	Glu	Ile	Cys	Leu	Leu	Lys	Ile	Ser	Ser	Gly	Leu	Leu	Glu	
			85					90						95		
Tyr	His	Ser	Tyr	Leu	Glu	Tyr	Met	Lys	Asn	Asn	Leu	Lys	Asp	Asn	Lys	
			100					105					110			
Lys	Asp	Lys	Ala	Arg	Val	Leu	Gln	Arg	Asp	Thr	Glu	Thr	Leu	Ile	His	
		115					120					125				
Ile	Phe	Asn	Gln	Glu	Val	Lys	Asp	Leu	His	Lys	Ile	Val	Leu	Pro	Thr	
	130					135					140					
Pro	Ile	Ser	Asn	Ala	Leu	Leu	Thr	Asp	Lys	Leu	Glu	Ser	Gln	Lys	Glu	
145					150					155					160	
Trp	Leu	Arg	Thr	Lys	Thr	Ile	Gln	Phe	Ile	Leu	Lys	Ser	Leu	Glu	Glu	
			165						170					175		
Phe	Leu	Lys	Val	Thr	Leu	Arg	Ser	Thr	Arg	Gln	Thr					
			180					185								

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Pro Leu Ala Glu Leu Ser Gly Asp His Asp Phe Gln Leu Phe Leu
1 5 10 15

His Lys Asn Leu Glu Phe Thr Arg Lys Ile Arg Gly Asp Val Ala Ala
20 25 30

Leu Gln Arg Ala Val Cys Asp Thr Phe Gln Leu Cys Thr Glu Glu Glu
35 40 45

Leu Gln Leu Val Gln Pro Asp Pro His Leu Val Gln Ala Pro Leu Asp
50 55 60

Gln Cys His Lys Arg Gly Phe Gln Ala Glu Val Cys Phe Thr Gln Ile
65 70 75 80

Arg Ala Gly Leu His Ala Tyr His Asp Ser Leu Gly Ala Val Leu Arg
85 90 95

Leu Leu Pro Asn His Thr Thr Leu Val Glu Thr Leu Gln Leu Asp Ala
100 105 110

Ala Asn Leu Ser Ser Asn Ile Gln Gln Gln Met Glu Asp Leu Gly Leu
115 120 125

Asp Thr Val Thr Leu Pro Ala Glu Gln Arg Ser Pro Pro Pro Thr Phe
130 135 140

Ser Gly Pro Phe Gln Gln Gln Val Gly Gly Phe Phe Ile Leu Ala Asn
145 150 155 160

Phe Gln Arg Phe Leu Glu Thr Ala Tyr Arg Ala Leu Arg His Leu Ala
165 170 175

Arg Leu

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys Asp Leu Leu
1 5 10 15

Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu Cys Phe Arg
20 25 30

